



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Botella, Jose Ramon
- (ii) TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
- (iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
- (B) STREET: 100 Thanet Circle, Suite 306
- (C) CITY: Princeton
- (D) STATE: NJ
- (E) COUNTRY: USA
- (F) ZIP: 08540-3662

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 09/043,627
- (B) FILING DATE: 20-MAR-1998
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/AU96/00591
- (B) FILING DATE: 20-SEP-1996

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: AU PN5559
- (B) FILING DATE: 20-SEP-1995

(ix) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: AU PN9603
- (B) FILING DATE: 02-MAY-1996

(x) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bernstein, Scott N.
- (B) REGISTRATION NUMBER: 38,827
- (C) REFERENCE/DOCKET NUMBER: 3573-11US

(xi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 609-924-8555
- (B) TELEFAX: 609-924-3036

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG ATG GGG TTT GCG GAG AAC CAG CTT TCG CTG GAG TTA ATA CGT GAG	48
Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu	
1 5 10 15	
TGG ATC AAG AAT CAC CCG GAG GCC TCC ATT TGC TCG GCG GAG GGC CTG	96
Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu	
20 25 30	
CCG CAG TTC ATG GAG ATC GCC AAT TTC CAA GAC TAC CAT GGC TTG CCG	144
Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
GCT TTT CTG CAG GGA ATC GCG AAA TTG ATG GAG AAA GTG AGA GGA GGA	192
Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly	
50 55 60	
AGG GTC AAA TTC GAT CCG AAC CGC GTG GTG ATG AGC GGC GGA GGC ACT	240
Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Thr	
65 70 75 80	
GGA GCG CAA GAA ACG CTC GCG TTT TGT CTC GCT GAC CCT GGC GAC GCC	288
Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala	
85 90 95	
TTC CTC GTC CCA ACT CCG TAC TAT CCA GCA TTT AAT CGC GAT CTC CGG	336
Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg	
100 105 110	
TGG AGA ACG GGC GTC GAG CTC CTC CCG GTT CAC TGC AAG AGC TCT AAT	384
Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn	
115 120 125	
CAC TTC AGA GTC ACC AAA ACG GCG CTA GAA TCG GCA TAC GAG AAG GCG	432
His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala	
130 135 140	
CGA AAG GAT AAC ATC AGA GTA AAA GGA GTA CTG ATA ACC AAC CCA TCC	480
Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser	
145 150 155 160	
AAC CCG CTC GGC ACG ACC ATG GAT AAA CAC ACG CTA CAG ACC CTC GTG	528
Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val	
165 170 175	
AAA TTC GTA AAC GAA AGG AGA ATC CAC CTA GTC TGC GAC GAG TTA TAC	576
Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr	
180 185 190	
GGC GCA ACC ATC TTT AGG GAG CCC AGG TTC GTC AGC ATC TCC GAG GTA	624
Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val	
195 200 205	

ATA GAA GAG GAC CCG AAC TGC GAC AAG AAT CTG ATC CAC ATT GCG TAC Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr 210 215 220	672
AGT CTC TCA AAG GAC TTC GGT CTC CCC GGA TTC CGA GTC GGG ATC GTG Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val 225 230 235 240	720
TAT TCC TAC AAC GAC ACG GTG GTT AGT TGC GCA CGC AGA ATG TCG AGC Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser 245 250 255	768
TTC GGC CTC GTC TCG TCG CAG ACA CAG TAC CTA CTG GCC GCC ATG CTA Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu 260 265 270	816
TCC GGC GAA GAA TTT TTG CCA ACA TTA CTG ACT GAA AGC GCG AAG AGT Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser 275 280 285	864
CTG TCG GAG AGC CAC AGG ATC TTC TCT TCC GGC CTT GAG GAA GTC GAC Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp 290 295 300	912
ATC CGC TGC TTG GAC GGC AAT GCC GGG GTC TTC TGC TGG ATG GAC CTA Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu 305 310 315 320	960
CGG CAC CTC CTC AAA GAA GCC ACC GAA GAC GGC GAG CTC GAG CTG TGG Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp 325 330 335	1008
CGC GTG ATA GTG AAC AAT GTC AAG CTC AAT GTG TCC CCC GGT TCG TCG Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser 340 345 350	1056
TTT TAT TGC GCC GAG CCA GGT TGG Phe Tyr Cys Ala Glu Pro Gly Trp 355 360	1080

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu 1 5 10 15
Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu 20 25 30
Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro 35 40 45

Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
 50 55 60

Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
 65 70 75 80

Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95

Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
 100 105 110

Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
 115 120 125

His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
 130 135 140

Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
 145 150 155 160

Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
 165 170 175

Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr
 180 185 190

Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
 195 200 205

Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
 210 215 220

Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
 225 230 235 240

Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
 245 250 255

Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
 260 265 270

Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
 275 280 285

Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
 290 295 300

Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
 305 310 315 320

Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
 325 330 335

Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350

Phe Tyr Cys Ala Glu Pro Gly Trp
 355 360

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAG ATG GGC CTT GCT GAG AAT CAG CTT TGC TTT AAT TTA ATT CAC GAG Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu 1 5 10 15	48
TGG CCG CTG AAA AAC CCA GAA GCC TCC ATT TGT ACA ACA CAA GGA GCA Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala 20 25 30	96
GCT GAA TTC AGA GAT ATA GCT ATC TTT CAA GAT TAT CAT GGC TTG GCT Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala 35 40 45	144
GAA TTC AGA GAG GCT GTT GCA AAG TTT ATG GGG AAA GTG AGA AGA AAC Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn 50 55 60	192
AGA GCT TCA TTT GAC CCT GAT CGG ATT GTT ATG AGT GGA GGA GCA ACT Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr 65 70 75 80	240
GGA GCT CAT GAA ATG ATT GGT TTC TGT TTG GCT GAT CCT GGC GAT GCA Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala 85 90 95	288
TTC TTG GTT CCA ACT CCT TAT TAT CCA GGG TTT GAT AGA GAT TTG AGA Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg 100 105 110	336
TGG AGA ACG GGA GTC AAA CTC ATT CCA GTT GTC TGT GAA AGC TCA AAC Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn 115 120 125	384
GAT TAC CAG ATC ACC ATA GAA GCC CTG GAA GCT GCT TAT GAA ACC GCA Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala 130 135 140	432
CAA GAA GCT GAC ATC AAG GTA AAG GGT TTG GTC ATA ACC AAC CCA TCA Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser 145 150 155 160	480
AAC CCA CTG GGA ACA ATT ATT ACC AAG GAC ACA TTA GAA GCT CTA GTC Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val 165 170 175	528

ACC TTC ACC AAC CAC AAG AAC ATT CAT CTG GTG TGT GAT GAG ATA TAT Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr 180 185 190	576
GCT GGT TAC CGT CTT CAG CCC AGG GCC GAA TTC ACC AGC ATA GCC GAG Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu 195 200 205	624
ATA ATT GAA GAA GAT AAA ATT TGT TGC AAT CGT GAT CTC ATC CAC ATC Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile 210 215 220	672
ATT TAC AGT TTA TCC AAA GAC ATG GGA TTC CCT GGA TTT AGA GTT GGC Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly 225 230 235 240	720
ATT GTG TAT TCA TAC AAT GAT GCA GTG GTG AGT TGT GCT CGT AAG ATG Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met 245 250 255	768
TCG AGC TTC GGC CTA GTA TCT TCG CAA ACC CAG TAT CTG ATT GCA TCC Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser 260 265 270	816
ATG TTA GCA GAC GAT GAA TTT GTA GAC AAA TTT ATT GTA GAG AGC AGA Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg 275 280 285	864
AAG AGG CTG GCA ATG AGA CAT AGT TTT TTC ACA CAA AGA CTT GCT CAA Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln 290 295 300	912
GTA GGC ATT AAC TGT TTA AAA AGC AAT GCT GGT CTT TTT GTG TGG ATG Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met 305 310 315 320	960
GAT TTG CGT AGA CTG CTG AAA GAA CAG ACA TTT GAA GCA GAA ATG GTG Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val 325 330 335	1008
TTA TGG AGA GTA ATT ATA AAC GAA ATG AAA CTC AAT GTA TCT CCT GGT Leu Trp Arg Val Ile Ile Asn Glu Met Lys Leu Asn Val Ser Pro Gly 340 345 350	1056
TCG TCT TTC CAC TGC TCA GAA CCT GGC TGG TTC AGC GTC TGC TTC GCT Ser Ser Phe His Cys Ser Glu Pro Gly Trp Phe Ser Val Cys Phe Ala 355 360 365	1104

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu
 1 5 10 15

Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala
 20 25 30

Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala
 35 40 45

Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn
 50 55 60

Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr
 65 70 75 80

Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala
 85 90 95

Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg
 100 105 110

Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn
 115 120 125

Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala
 130 135 140

Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser
 145 150 155 160

Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val
 165 170 175

Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190

Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu
 195 200 205

Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile
 210 215 220

Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly
 225 230 235 240

Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met
 245 250 255

Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser
 260 265 270

Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg
 275 280 285

Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln
 290 295 300

Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met
 305 310 315 320

Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val
 325 330 335

Leu Trp Arg Val Ile Ile Asn Glu Met Lys Leu Asn Val Ser Pro Gly
 340 345 350

Ser Ser Phe His Cys Ser Glu Pro Gly Trp Phe Ser Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..1098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAG ATG GGT TTT GCT GAA AAT CAG CTT TGC TTT GAT TTG ATC GAG AAG Gln Met Gly Phe Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Lys 1 5 10 15	48
TGG GTT AAA AAG AAT CCC AAT GCT TCC ATC TGC ACA GCT GAA GGG GTT Trp Val Lys Lys Asn Pro Asn Ala Ser Ile Cys Thr Ala Glu Gly Val 20 25 30	96
GAA AAC TTC AAG CAC ATA GCC AAC TTC CAA GAC TAT CAT GGC CTG AAA Glu Asn Phe Lys His Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Lys 35 40 45	144
GAA TTT AGA CAG GAA GTT GCC AAG TTA ATG GGG AAG GCA AGA GGC GGC Glu Phe Arg Gln Glu Val Ala Lys Leu Met Gly Lys Ala Arg Gly Gly 50 55 60	192
AGA GTG ACG TTC GAC CCA GAG CGT ATT GTG ATG AGC GGG GGA GCG ACA Arg Val Thr Phe Asp Pro Glu Arg Ile Val Met Ser Gly Gly Ala Thr 65 70 75 80	240
GGC GCC AGC GAG ACG ATT ATG TTT TGC TTG GCG GAT CCA GGC GAT GCT Gly Ala Ser Glu Thr Ile Met Phe Cys Leu Ala Asp Pro Gly Asp Ala 85 90 95	288
CTT CTG GTT CCC ACT CCT TAC TAT CCT GGA TTC AAT AGG GAC CTG AGA Leu Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asn Arg Asp Leu Arg 100 105 110	336
TGG CGA ACC GGC GTC CAG ATT ATT CCC GTG CAA TGC AGC AGC TCA CAC Trp Arg Thr Gly Val Gln Ile Ile Pro Val Gln Cys Ser Ser Ser His 115 120 125	384

AAT TTT ACA GTA ACA CGG GAA GCC GTA GAG GCT GCG TAC CAG AAA GCT Asn Phe Thr Val Thr Arg Glu Ala Val Glu Ala Ala Tyr Gln Lys Ala 130 135 140	432
CAA GAA GCC AAC ATC AAT GTC ACA GGC TTG ATC ATC ACC AAC CCC TCG Gln Glu Ala Asn Ile Asn Val Thr Gly Leu Ile Ile Thr Asn Pro Ser 145 150 155 160	480
AAT CCG CTA GGC ACC ACC TTA GAC TCA CAA ACA CTC CAG AGC TTG GTC Asn Pro Leu Gly Thr Thr Leu Asp Ser Gln Thr Leu Gln Ser Leu Val 165 170 175	528
ATC TTC GTC AAC GAC AAG ACC ATC CAC CTG GTC TGC GAC GAA ATC TAT Ile Phe Val Asn Asp Lys Thr Ile His Leu Val Cys Asp Glu Ile Tyr 180 185 190	576
GCC GCC ACC GTC TTC AGC TCC CCG GAG TTC GTC AGC ATC GGG GAG ATC Ala Ala Thr Val Phe Ser Ser Pro Glu Phe Val Ser Ile Gly Glu Ile 195 200 205	624
ATC CAA GAA ATG GAC GTC AAC CGC GAC CTT ATC CAC ATC ATC TAC AGC Ile Gln Glu Met Asp Val Asn Arg Asp Leu Ile His Ile Ile Tyr Ser 210 215 220	672
TTG TCC AAA GAT ATG GGT CTC CCC GGT TTC CGG GTA GGT ATT GTG TAT Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr 225 230 235 240	720
TCC TAC AAC GAC GGT GTA TTA AGC TGC GGC CGG CGG ATG TCG AGC TTT Ser Tyr Asn Asp Gly Val Leu Ser Cys Gly Arg Arg Met Ser Ser Phe 245 250 255	768
GGG TTG GTC TCG TCA CAG ACT CAA TAT TTC CTG GCG ACA CTG CTG TCC Gly Leu Val Ser Ser Gln Thr Gln Tyr Phe Leu Ala Thr Leu Leu Ser 260 265 270	816
GAC GAC GAG TTC GTC GAT TAC TTC CTC CGG GAA AGC TCG AAG AGG CTG Asp Asp Glu Phe Val Asp Tyr Phe Leu Arg Glu Ser Ser Lys Arg Leu 275 280 285	864
GCG AGA AGA CAC CAT AAA CTC ACC AGA GGG CTG GAG CAA GTG GGG ATA Ala Arg Arg His His Lys Leu Thr Arg Gly Leu Glu Gln Val Gly Ile 290 295 300	912
AAG TGC TTG AAA AGC AAT GCC GGA CTT TTT GTG TGG ATG GAC CTG CGG Lys Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg 305 310 315 320	960
AGG CTC CTG GAA GGT CCA ACG TCG TTT GAT GCA GAA ATG AAG CTG TGG Arg Leu Leu Glu Gly Pro Thr Ser Phe Asp Ala Glu Met Lys Leu Trp 325 330 335	1008
CGG ACC ATC GTC AAC GAC GTG AAG CTG AAC GTG TCG CCG GGA TCT TCG Arg Thr Ile Val Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser 340 345 350	1056
TTC CAC GTG GCG GAG CCG GGG TGG TTC AGA GTA TGT TTC GCT Phe His Val Ala Glu Pro Gly Trp Phe Arg Val Cys Phe Ala 355 360 365	1098

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln	Met	Gly	Phe	Ala	Glu	Asn	Gln	Leu	Cys	Phe	Asp	Leu	Ile	Glu	Lys
1					5				10				15		
Trp	Val	Lys	Lys	Asn	Pro	Asn	Ala	Ser	Ile	Cys	Thr	Ala	Glu	Gly	Val
					20				25				30		
Glu	Asn	Phe	Lys	His	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Lys
					35			40				45			
Glu	Phe	Arg	Gln	Glu	Val	Ala	Lys	Leu	Met	Gly	Lys	Ala	Arg	Gly	Gly
					50		55			60					
Arg	Val	Thr	Phe	Asp	Pro	Glu	Arg	Ile	Val	Met	Ser	Gly	Gly	Ala	Thr
					65		70			75			80		
Gly	Ala	Ser	Glu	Thr	Ile	Met	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala
					85			90			95				
Leu	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Gly	Phe	Asn	Arg	Asp	Leu	Arg
					100			105			110				
Trp	Arg	Thr	Gly	Val	Gln	Ile	Ile	Pro	Val	Gln	Cys	Ser	Ser	Ser	His
					115			120			125				
Asn	Phe	Thr	Val	Thr	Arg	Glu	Ala	Val	Glu	Ala	Ala	Tyr	Gln	Lys	Ala
					130		135			140					
Gln	Glu	Ala	Asn	Ile	Asn	Val	Thr	Gly	Leu	Ile	Ile	Thr	Asn	Pro	Ser
					145			150			155			160	
Asn	Pro	Leu	Gly	Thr	Thr	Leu	Asp	Ser	Gln	Thr	Leu	Gln	Ser	Leu	Val
					165			170			175				
Ile	Phe	Val	Asn	Asp	Lys	Thr	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr
					180			185			190				
Ala	Ala	Thr	Val	Phe	Ser	Ser	Pro	Glu	Phe	Val	Ser	Ile	Gly	Glu	Ile
					195			200			205				
Ile	Gln	Glu	Met	Asp	Val	Asn	Arg	Asp	Leu	Ile	His	Ile	Ile	Tyr	Ser
					210		215			220					
Leu	Ser	Lys	Asp	Met	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	Tyr
					225			230			235			240	
Ser	Tyr	Asn	Asp	Gly	Val	Leu	Ser	Cys	Gly	Arg	Arg	Met	Ser	Ser	Phe
					245			250			255				
Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Ser
					260			265			270				

Asp Asp Glu Phe Val Asp Tyr Phe Leu Arg Glu Ser Ser Lys Arg Leu
 275 280 285

Ala Arg Arg His His Lys Leu Thr Arg Gly Leu Glu Gln Val Gly Ile
 290 295 300

Lys Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg
 305 310 315 320

Arg Leu Leu Glu Gly Pro Thr Ser Phe Asp Ala Glu Met Lys Leu Trp
 325 330 335

Arg Thr Ile Val Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser
 340 345 350

Phe His Val Ala Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1096 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAG ATG GGC CTT GCC GAG AAT CAG CTT TGC TTT GAT TTG ATC GAA GAC Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Asp	48
1 5 10 15	
TGG ATT CGC AAA AAT CCC TAT GCC TCC ATT TGT ACT GCT GAA GGA GTT Trp Ile Arg Lys Asn Pro Tyr Ala Ser Ile Cys Thr Ala Glu Gly Val	96
20 25 30	
GAT GAG TTC AAG GAG ATT GCA AAC TTT CAA GAT TAT CAT GGC TTG CCA Asp Glu Phe Lys Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro	144
35 40 45	
GAG TTT AGA AAG GCT GTG GCA AAG TTT ATG GGA AAA GTG AGA GGT GGA Glu Phe Arg Lys Ala Val Ala Lys Phe Met Gly Lys Val Arg Gly Gly	192
50 55 60	
AGA GTA ACA TTT GAT CCA GAC CGT ATA GTC ATG GGC GGT GGA GTT ACA Arg Val Thr Phe Asp Pro Asp Arg Ile Val Met Gly Gly Val Thr	240
65 70 75 80	
GGC GCA AAC GAG CAA ATC ATC TTC TGT TTA GCC GAC CCT GGC GAT GCT Gly Ala Asn Glu Gln Ile Ile Phe Cys Leu Ala Asp Pro Gly Asp Ala	288
85 90 95	

TTT CTT GTT CCC TCA CCT TAT TAT CCA GCA TTT GAC CGG GAC CTG GGA Phe Leu Val Pro Ser Pro Tyr Tyr Pro Ala Phe Asp Arg Asp Leu Gly 100 105 110	336
TGG CGC ACT GGA GGT GAA ATA GTT CCT GTT CCC TGT GAC AGC TCA ACC Trp Arg Thr Gly Gly Glu Ile Val Pro Val Pro Cys Asp Ser Ser Thr 115 120 125	384
AAT TTC CAG ATA ACC AGA GAT GCA TTG GAA GAA GCA TAT GAA AAA GCT Asn Phe Gln Ile Thr Arg Asp Ala Leu Glu Ala Tyr Glu Lys Ala 130 135 140	432
CGA GAA GCC AAC ATT AAT ATT AAA GGC TTG ATC ATA ACA AAC CCT TCA Arg Glu Ala Asn Ile Asn Ile Lys Gly Leu Ile Ile Thr Asn Pro Ser 145 150 155 160	480
AAC CCA CTT GGC ATC ACC CTA GAC AGA GAT ACT CTT AAA AGC CTA GTG Asn Pro Leu Gly Ile Thr Leu Asp Arg Asp Thr Leu Lys Ser Leu Val 165 170 175	528
AGC TTC ATC GAT GAA AAG AAC ATT CAC TTT GTC TGC GAT GAA ATC TAT Ser Phe Ile Asp Glu Lys Asn Ile His Phe Val Cys Asp Glu Ile Tyr 180 185 190	576
GCT GCC ACT CTC TTC TGT CCA CCC AAG TTC GTA AGC GTC GCT GAA GTG Ala Ala Thr Leu Phe Cys Pro Pro Lys Phe Val Ser Val Ala Glu Val 195 200 205	624
ATC CAA GAA ATG GAC TGT AAT CTT GAT CTC ATC CAC ATT GTT TAC AGT Ile Gln Glu Met Asp Cys Asn Leu Asp Leu Ile His Ile Val Tyr Ser 210 215 220	672
TTG TCT AAG GAC ATG GGC CTC CCT GGC TTT AGG GTT GGC ATT GTT TAT Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr 225 230 235 240	720
TCT TAT AAT GAT GCA GTT GTG AGT TGT ATC CGC AAG ATG TCA AGC TTC Ser Tyr Asn Asp Ala Val Val Ser Cys Ile Arg Lys Met Ser Ser Phe 245 250 255	768
GGT TTG GTA TCC TCA CAA ACT CAA TAT TTA CTC GCT TCA ATG CTT TCT Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Ser 260 265 270	816
GAT GAT GAA TTT GTG GAA AAG TTT CTA GCG GAA AGC TCA AAG AGG CTG Asp Asp Glu Phe Val Glu Lys Phe Leu Ala Glu Ser Ser Lys Arg Leu 275 280 285	864
GCA AAA AGG TAC CAT ATT TTC ACA AAG AGA CTT GAG AAA GTG GGG ATT Ala Lys Arg Tyr His Ile Phe Thr Lys Arg Leu Glu Lys Val Gly Ile 290 295 300	912
AAC TGC TTG AAG GGA AAT GCA GGT CTT TTC TTC TGG ATG GAT TTG CGA Asn Cys Leu Lys Gly Asn Ala Gly Leu Phe Phe Trp Met Asp Leu Arg 305 310 315 320	960
CAC CTC CTT CAA CAA GAA ACA GTT GAT GCC GAA ATG AAG CTA TGG GGC His Leu Leu Gln Gln Glu Thr Val Asp Ala Glu Met Lys Leu Trp Gly 325 330 335	1008

ACG ATT TTG AAC GAT GTG AAA CTT AAC GTT TCA CCA GGC TCT TCC TTT	1056
Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe	
340	345
350	
CAT TGC CAG GAG CCT GGT TGG TTC AGA GTC TGC TTC GCT G	1096
His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala	
355	360
365	

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asp Leu Ile Glu Asp			
1	5	10	15
Trp Ile Arg Lys Asn Pro Tyr Ala Ser Ile Cys Thr Ala Glu Gly Val			
20	25		30
Asp Glu Phe Lys Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro			
35	40		45
Glu Phe Arg Lys Ala Val Ala Lys Phe Met Gly Lys Val Arg Gly Gly			
50	55		60
Arg Val Thr Phe Asp Pro Asp Arg Ile Val Met Gly Gly Gly Val Thr			
65	70		75
80			
Gly Ala Asn Glu Gln Ile Ile Phe Cys Leu Ala Asp Pro Gly Asp Ala			
85	90		95
Phe Leu Val Pro Ser Pro Tyr Tyr Pro Ala Phe Asp Arg Asp Leu Gly			
100	105		110
Trp Arg Thr Gly Gly Glu Ile Val Pro Val Pro Cys Asp Ser Ser Thr			
115	120		125
Asn Phe Gln Ile Thr Arg Asp Ala Leu Glu Glu Ala Tyr Glu Lys Ala			
130	135		140
Arg Glu Ala Asn Ile Asn Ile Lys Gly Leu Ile Ile Thr Asn Pro Ser			
145	150		155
160			
Asn Pro Leu Gly Ile Thr Leu Asp Arg Asp Thr Leu Lys Ser Leu Val			
165	170		175
Ser Phe Ile Asp Glu Lys Asn Ile His Phe Val Cys Asp Glu Ile Tyr			
180	185		190
Ala Ala Thr Leu Phe Cys Pro Pro Lys Phe Val Ser Val Ala Glu Val			
195	200		205
Ile Gln Glu Met Asp Cys Asn Leu Asp Leu Ile His Ile Val Tyr Ser			
210	215		220

Leu Ser Lys Asp Met Gly Leu Pro Gly Phe Arg Val Gly Ile Val Tyr
 225 230 235 240
 Ser Tyr Asn Asp Ala Val Val Ser Cys Ile Arg Lys Met Ser Ser Phe
 245 250 255
 Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Ser
 260 265 270
 Asp Asp Glu Phe Val Glu Lys Phe Leu Ala Glu Ser Ser Lys Arg Leu
 275 280 285
 Ala Lys Arg Tyr His Ile Phe Thr Lys Arg Leu Glu Lys Val Gly Ile
 290 295 300
 Asn Cys Leu Lys Gly Asn Ala Gly Leu Phe Phe Trp Met Asp Leu Arg
 305 310 315 320
 His Leu Leu Gln Gln Glu Thr Val Asp Ala Glu Met Lys Leu Trp Gly
 325 330 335
 Thr Ile Leu Asn Asp Val Lys Leu Asn Val Ser Pro Gly Ser Ser Phe
 340 345 350
 His Cys Gln Glu Pro Gly Trp Phe Arg Val Cys Phe Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAG ATG GGA TTT GGG GAA AAT CTG CTT TGC TTT GAT TTA GTT CAA GAA	48
Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu	
1 5 10 15	
TGG GTC TTA AGC AAC CCA GAA GCC TCT ATC TGC ACT GCC GAA GGT ATA	96
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile	
20 25 30	
AGT GAT TTC AGA GAT ATC GCT ATC TTT CAG GAT TAT CAC GGC TTG CCA	144
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro	
35 40 45	
GAG TTC AGA AAT GCT GTT GCA AAT TTT ATG GCA AGA GTG AGA GGG AAT	192
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn	
50 55 60	

AGA GTC AAA TAC GAC CCT GAT CGA ATT GTT ATG AGC GGT GGA GCA ACC Arg Val Lys Tyr Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr 65 70 75 80	240
GGA GCA CAT GAG ACG GTT GCC TTT TGT TTG GCT GAT CCC GGT GAA GCA Gly Ala His Glu Thr Val Ala Phe Cys Leu Ala Asp Pro Gly Glu Ala 85 90 95	288
TTT TTG GGT GCC ACT CCT TAC TAT CCA GGA TTT GGT CGA GAT TTG AGA Phe Leu Gly Ala Thr Pro Tyr Tyr Pro Gly Phe Gly Arg Asp Leu Arg 100 105 110	336
TGG AGA ACA GGA GTT CAA CTT TTT CCA GTT GTG TGT GAC AGT TCT AAC Trp Arg Thr Gly Val Gln Leu Phe Pro Val Val Cys Asp Ser Ser Asn 115 120 125	384
AAT TTC AAG ATT ACA AGA GAA GCC GTG GAA GCA GCA TAT GAA AAA GCT Asn Phe Lys Ile Thr Arg Glu Ala Val Glu Ala Ala Tyr Glu Lys Ala 130 135 140	432
CAA GAA GAC CAC ATC AGA ATC AAG GGT TTG GTC CTC ACA AAT CCA TCG Gln Glu Asp His Ile Arg Ile Lys Gly Leu Val Leu Thr Asn Pro Ser 145 150 155 160	480
AAC CCG CTG GGG ACT TGT TTG GAC AGA GAA ACA CTA AGA AGT TTA GTA Asn Pro Leu Gly Thr Cys Leu Asp Arg Glu Thr Leu Arg Ser Leu Val 165 170 175	528
AGC TTC ATT AAT GAA AAG AAC ATC CAC TTA GTC TGC GAC GAG ATT TAT Ser Phe Ile Asn Glu Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr 180 185 190	576
GCT GCC ACA ATC TTC ATG GGC CAG CCC GAT TTC ATT AGC ATC TCT GAA Ala Ala Thr Ile Phe Met Gly Gln Pro Asp Phe Ile Ser Ile Ser Glu 195 200 205	624
ATT ATA GAA GAA GAT ATT CAC TGC AAT CGC AAT CTC ATC CAC CTT GTT Ile Ile Glu Glu Asp Ile His Cys Asn Arg Asn Leu Ile His Leu Val 210 215 220	672
TAC AGT CTT TCA AAG GAT CTG GGG TTC CCA GGC TTT AGG GTC GGC ATT Tyr Ser Leu Ser Lys Asp Leu Gly Phe Pro Gly Phe Arg Val Gly Ile 225 230 235 240	720
ATA TAC TCA TAC AAC GAT ACA GTT GTG AGT TGC GCC TGC AAA ATG TCA Ile Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Cys Lys Met Ser 245 250 255	768
AGC TTT GGA CTT GTA TCA TCA CAA ACT CAA CAT TTA ATC GCT TCA ATG Ser Phe Gly Leu Val Ser Ser Gln Thr Gln His Leu Ile Ala Ser Met 260 265 270	816
TTA TCA GAT GAT GAA TTT GTG GAT AGG TTC ATT ACT GAG AGT GCT AAA Leu Ser Asp Asp Glu Phe Val Asp Arg Phe Ile Thr Glu Ser Ala Lys 275 280 285	864
AGG CTT GCA AAA AGG CAC AGA GCC TTC ACA TGG GGG CTA TCT CAA GTA Arg Leu Ala Lys Arg His Arg Ala Phe Thr Trp Gly Leu Ser Gln Val 290 295 300	912

GGC ATT GGT TGT TTG AAG AGC AAT GCG GGG CTA TTT TTC TGG ATG GAT Gly Ile Gly Cys Leu Lys Ser Asn Ala Gly Leu Phe Phe Trp Met Asp 305 310 315 320	960
TTG CAT CAT CTC CTC AAG GAG CAA ACT GAT GAA GCA GAG ATA GAA CTG Leu His His Leu Leu Lys Glu Gln Thr Asp Glu Ala Glu Ile Glu Leu 325 330 335	1008
TGG AAA GTG ATA ATC AAC GAA GTT AAA TTA AAT GTT TCT CCG GGT TCT Trp Lys Val Ile Ile Asn Glu Val Lys Leu Asn Val Ser Pro Gly Ser 340 345 350	1056
TCC TTT CAT TGC GCT AAT CCA GGA TGG TTT CGG GTT TGT TTC GCC AAC Ser Phe His Cys Ala Asn Pro Gly Trp Phe Arg Val Cys Phe Ala Asn 355 360 365	1104
ATG GAC GAA Met Asp Glu 370	1113

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Met Gly Phe Gly Glu Asn Leu Leu Cys Phe Asp Leu Val Gln Glu 1 5 10 15
Trp Val Leu Ser Asn Pro Glu Ala Ser Ile Cys Thr Ala Glu Gly Ile 20 25 30
Ser Asp Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Pro 35 40 45
Glu Phe Arg Asn Ala Val Ala Asn Phe Met Ala Arg Val Arg Gly Asn 50 55 60
Arg Val Lys Tyr Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr 65 70 75 80
Gly Ala His Glu Thr Val Ala Phe Cys Leu Ala Asp Pro Gly Glu Ala 85 90 95
Phe Leu Gly Ala Thr Pro Tyr Tyr Pro Gly Phe Gly Arg Asp Leu Arg 100 105 110
Trp Arg Thr Gly Val Gln Leu Phe Pro Val Val Cys Asp Ser Ser Asn 115 120 125
Asn Phe Lys Ile Thr Arg Glu Ala Val Glu Ala Ala Tyr Glu Lys Ala 130 135 140
Gln Glu Asp His Ile Arg Ile Lys Gly Leu Val Leu Thr Asn Pro Ser 145 150 155 160

Asn Pro Leu Gly Thr Cys Leu Asp Arg Glu Thr Leu Arg Ser Leu Val
 165 170 175
 Ser Phe Ile Asn Glu Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
 180 185 190
 Ala Ala Thr Ile Phe Met Gly Gln Pro Asp Phe Ile Ser Ile Ser Glu
 195 200 205
 Ile Ile Glu Glu Asp Ile His Cys Asn Arg Asn Leu Ile His Leu Val
 210 215 220
 Tyr Ser Leu Ser Lys Asp Leu Gly Phe Pro Gly Phe Arg Val Gly Ile
 225 230 235 240
 Ile Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Cys Lys Met Ser
 245 250 255
 Ser Phe Gly Leu Val Ser Ser Gln Thr Gln His Leu Ile Ala Ser Met
 260 265 270
 Leu Ser Asp Asp Glu Phe Val Asp Arg Phe Ile Thr Glu Ser Ala Lys
 275 280 285
 Arg Leu Ala Lys Arg His Arg Ala Phe Thr Trp Gly Leu Ser Gln Val
 290 295 300
 Gly Ile Gly Cys Leu Lys Ser Asn Ala Gly Leu Phe Phe Trp Met Asp
 305 310 315 320
 Leu His His Leu Leu Lys Glu Gln Thr Asp Glu Ala Glu Ile Glu Leu
 325 330 335
 Trp Lys Val Ile Ile Asn Glu Val Lys Leu Asn Val Ser Pro Gly Ser
 340 345 350
 Ser Phe His Cys Ala Asn Pro Gly Trp Phe Arg Val Cys Phe Ala Asn
 355 360 365
 Met Asp Glu
 370

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAYTTYGAYG GNTGGAARGC

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCRTCCATRT TNGCRAARCA

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CARATGGGNY TNGCNGARAA

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCRAARCANA CNCKRAACCA

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTGATCARA TGGGNYTNGC NGARAA

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCTGCAGCR AARCANACNC KRAACCA

27